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RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: ___09 | 765,061 C___

Source: ___OIPE___

Date Processed by STIC: ___1|7|03___

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO **REDUCE** ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>, **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. **Hand Carry directly to:**
    U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
            Or
    U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
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Revised 01/29/2002

OIPE

Does Not Comply
Corrected Diskette Needed

RAW SEQUENCE LISTING   DATE: 01/07/2003
PATENT APPLICATION: **US/09/765,061C**   TIME: 14:04:21

Input Set : **A:\SQ 09765061.txt**
Output Set: **N:\CRF4\01072003\I765061C.raw**

```
   3 <110> APPLICANT: The Board of Regents of the University of Texas System
   5 <120> TITLE OF INVENTION: MUTATIONS IN A NOVEL PHOTORECEPTOR-PINEAL GENE ON 17P
   6       CAUSE LEBER CONGENITAL AMAUROSIS (LCA4)
   8 <130> FILE REFERENCE: 96606/16UTL
  10 <140> CURRENT APPLICATION NUMBER: 09/765,061C
C--> 11 <141> CURRENT FILING DATE: 2003-01-07
  13 <150> PRIOR APPLICATION NUMBER: 60/331362
  14 <151> PRIOR FILING DATE: 2001-01-04
  16 <160> NUMBER OF SEQ ID NOS: (10)  — but seq. nos. were designated as 79 through 88
  18 <170> SOFTWARE: PatentIn version 3.1
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ERRORED SEQUENCES

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  20 <210> SEQ ID NO: 79
  21 <211> LENGTH: 34
  22 <212> TYPE: DNA
  23 <213> ORGANISM: Homo sapiens
  25 <220> FEATURE:
  26 <221> NAME/KEY: exon
  27 <222> LOCATION: (1)..(34)
  28 <223> OTHER INFORMATION: Donor Splice Site: Residue 1-10 are the exonic sequence
  29       and Resi
  30       dues 11-34 are the intronic sequence
  33 <400> SEQUENCE: 79
E--> 34 cgg atc ccg agt gag tgg ggc cct ccg gag cag a
  35      34
  38 <210> SEQ ID NO: 80
  39 <211> LENGTH: 35
  40 <212> TYPE: DNA
  41 <213> ORGANISM: Homo sapiens
  43 <220> FEATURE:
  44 <221> NAME/KEY: exon
  45 <222> LOCATION: (1)..(35)
  46 <223> OTHER INFORMATION: Acceptor Splice Site: Residues 1-25 are the intronic
  47       sequence an
  48       d Residues 26-35 are the exonic sequence.
  51 <400> SEQUENCE: 80
E--> 52 cag agt gca ccg tct cgg tga cta ggt gat ctt tc
  53      35
  56 <210> SEQ ID NO: 81
  57 <211> LENGTH: 35
  58 <212> TYPE: DNA
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nucleotides must be in groups of 10 bases, with enumeration
on the right margin — per § 1.822 (c)(2) +(6) of the New Rules
—if wrapped nucleit, see error summary
sheet item 1

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      59 <213> ORGANISM: Homo sapiens
      61 <220> FEATURE:
      62 <221> NAME/KEY: exon
      63 <222> LOCATION: (1)..(35)
      64 <223> OTHER INFORMATION: Donor Splice Site: Residue 1-10 are the exonic sequence
      65      and Resi
      66      dues 11-35 are the intronic sequence
      69 <400> SEQUENCE: 81
E-->  70 csa cac cat cgt aag tag gcc ctg cgc gcc tgt ct
      71      35
      74 <210> SEQ ID NO: 82
      75 <211> LENGTH: 35
      76 <212> TYPE: DNA
      77 <213> ORGANISM: Homo sapiens
      79 <220> FEATURE:
      80 <221> NAME/KEY: exon
      81 <222> LOCATION: (1)..(35)
      82 <223> OTHER INFORMATION: Acceptor Splice Site: Residues 1-25 are the intronic
      83      sequence an
      84      d Residues 26-35 are the exonic sequence.
      87 <400> SEQUENCE: 82
E-->  88 gcc atc cat ccg ttt atc ccc aca gca cac ggg gg
      89      35
      92 <210> SEQ ID NO: 83
      93 <211> LENGTH: 35
      94 <212> TYPE: DNA
      95 <213> ORGANISM: Homo sapiens
      97 <220> FEATURE:
      98 <221> NAME/KEY: exon
      99 <222> LOCATION: (1)..(35)
     100 <223> OTHER INFORMATION: Donor Splice Site: Residue 1-10 are the exonic sequence
     101      and Resi
     102      dues 11-35 are the intronic sequence
     105 <400> SEQUENCE: 83
E--> 106 gct gct gca ggt ggg gct ggg gtt ggc agg gct gg
     107      35
     110 <210> SEQ ID NO: 84
     111 <211> LENGTH: 35
     112 <212> TYPE: DNA
     113 <213> ORGANISM: Homo sapiens
     115 <220> FEATURE:
     116 <221> NAME/KEY: exon
     117 <222> LOCATION: (1)..(35)
     118 <223> OTHER INFORMATION: Acceptor Splice Site: Residues 1-25 are the intronic
     119      sequence an
     120      d Residues 26-35 are the exonic sequence.
     123 <400> SEQUENCE: 84
E--> 124 cac tga cct gca gct ctg ggg cca ggt tga tgc cc
     125      35
```

RAW SEQUENCE LISTING   DATE: 01/07/2003
PATENT APPLICATION: US/09/765,061C   TIME: 14:04:21

Input Set : A:\SQ 09765061.txt
Output Set: N:\CRF4\01072003\I765061C.raw

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       130 <212> TYPE: DNA
       131 <213> ORGANISM: Homo sapiens
       133 <220> FEATURE:
       134 <221> NAME/KEY: exon
       135 <222> LOCATION: (1)..(35)
       136 <223> OTHER INFORMATION: Donor Splice Site: Residue 1-10 are the exonic sequence
       137       and Resi
       138       dues 11-35 are the intronic sequence
       141 <400> SEQUENCE: 85
E-->   142 gca gac caa ggt cag agg ccg ctg gcc acg ggg tg
       143      35
       146 <210> SEQ ID NO: 86
       147 <211> LENGTH: 35
       148 <212> TYPE: DNA
       149 <213> ORGANISM: Homo sapiens
       151 <220> FEATURE:
       152 <221> NAME/KEY: exon
       153 <222> LOCATION: (1)..(35)
       154 <223> OTHER INFORMATION: Acceptor Splice Site: Residues 1-25 are the intronic
       155       sequence an
       156       d Residues 26-35 are the exonic sequence.
       159 <400> SEQUENCE: 86
E-->   160 cat ggc tga cct tct ccc tgg gca gga gaa gcc rt
       161      35
       164 <210> SEQ ID NO: 87
       165 <211> LENGTH: 35
       166 <212> TYPE: DNA
       167 <213> ORGANISM: Homo sapiens
       169 <220> FEATURE:
       170 <221> NAME/KEY: exon
       171 <222> LOCATION: (1)..(35)
       172 <223> OTHER INFORMATION: Donor Splice Site: Residue 1-10 are the exonic sequence
       173       and Resi
       174       dues 11-35 are the intronic sequence
       177 <400> SEQUENCE: 87
E-->   178 cac cac cca ggt gcg cgg ggc tgc agg ggc gga ca
       179      35
       182 <210> SEQ ID NO: 88
       183 <211> LENGTH: 35
       184 <212> TYPE: DNA
       185 <213> ORGANISM: Homo sapiens
       187 <220> FEATURE:
       188 <221> NAME/KEY: exon
       189 <222> LOCATION: (1)..(35)
       190 <223> OTHER INFORMATION: Acceptor Splice Site: Residues 1-25 are the intronic
       191       sequence an
       192       d Residues 26-35 are the exonic sequence.
```

```
       195 <400> SEQUENCE: 88
E--> 196 gct gga tgc tcc ctg ctc ccc aca ggc atc gtg aa
       197    35
```

VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/765,061C**

DATE: 01/07/2003
TIME: 14:04:22

Input Set : **A:\SQ 09765061.txt**
Output Set: **N:\CRF4\01072003\I765061C.raw**

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:34 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:34 SEQ:79
L:52 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:35 SEQ:80
L:70 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:35 SEQ:81
L:88 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:35 SEQ:82
L:106 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:35 SEQ:83
L:124 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:35 SEQ:84
L:142 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:35 SEQ:85
L:160 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:35 SEQ:86
L:178 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:35 SEQ:87
L:196 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:35 SEQ:88

OIPE

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09|765,061C

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ✓ Wrapped Nucleics
    Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ___ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ___ Misaligned Amino
    Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ___ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ___ Variable Length

Sequence(s)___contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ___ PatentIn 2.0
    "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ___ Skipped Sequences
    (OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ___ Skipped Sequences
    (NEW RULES)

Sequence(s) _____ missing. If Intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ___ Use of n's or Xaa's
    (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.

10 ___ Invalid <213>
    Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ___ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ___ PatentIn 2.0
    "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ___ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001